SEQ ID NO:1 FIGURE 1

CCGCGAGGTGCGCGGTCTCTTTAAGGCGGGTCCTGGTGGTTTCTGTTTCCTGAAGGAAGTGACGGGGGTGGGATTGAATGAAAAGTGCAAAACACAGGCTCGCAGCGCTGGA GGGCGCCTGCTGAGCGCTACCCACGTGCGTCCGCGCCACCTCGCGGGCGACCCCG CGGCCAAGGCCCCGGCGGAGCGGCTCCCGGGCGCCCCGAACTAGCCCCCAACTTT CGGCAGCGCCCCGGGGATGCGCCTTCCCGGGGTACCCCTGGCGCCCCTGCGCT GCGGGTCCGCGTGCCGGACGGCCAGGTGACCGAGGAGAGCCTGCAGGCGG ACAGCGACGCGACAGCATCAGCCTCGAGCTGCGCAAGCCCGACGCCACCCTCGTC TCCTTCACCGCCGACTTCAAGAAGGATGTGAAGGTCTTCCGGGCCCTGATCCTGGGG GAGCTGGAGAAGGGGCAGAGTCAGTTCCAGGCCCTCTGCTTTGTCACCCAGCTGCA GCACAATGAGATCATCCCCAGTGAGGCCATGGCCAAGCTCCGGCAGAAAAATCCCC GGGCAGTGCGGCAGGCGGAGGAGGTTCGGGGTCTGGAGCATCTGCACATGGATGTC GCTGTCAACTTCAGCCAGGGGGCCCTGCTGAGCCCCCATCTCCACAACGTGTGTGCC AGGTGTGGACAGTTCTGTGTTCGAGGCTCTGCCCAAGGCCTCAGAGCAGGCGGAGC TGCCTCGCTGCAGGCAGGTGGGGGACCGCGGGAAGCCCTGCGTCTGCCACTATGGCACGCCCTACAAGTGTGGCATCCGCAGCTGCCAGAAGAGCTACAGCTTCGACTTCTAC GTGCCCCAGAGGCAGCTGTGTCTCTGGGATGAGGATCCCTACCCAGGCTAGGGTGG GAGCAACCTGGGCGGGTGGCTGCTCTGGGCCCACTGCTCTTCACCAGCCACTAGAGG GGGTGCAACCCCACCTGAGGCCTTATTTCCCTCCCTCCCACTCCCCTGGCCCTA GAGCCTGGGCCCCTCTGGCCCCATCTCACATGACTGTGAAGGGGGTGTGGCATGGCA GGAGAGAAGGGCTCCCAGATCTACACCCCTCCCTCCTGCATCTCCCCTGGAGTGTT ${\tt CACTTGCAAGCTGCCAAAACATGATGGCCTCTGGTTGTTCTGTTGAACTCCTTGAAC}$ GTTTAGACCCTAAAAGGAGTCTATACCTGGACACCCACCTCCCCAGACACACTCCC TTCCCCATGCACACATCTGGAAGGAGCTGGCCCCTCAGTCCCTTCCTACTCCCCAAC AAGGGGCTCACTATCCCCAAAGAAGGAGCTGTTGGGGACCCACGACGCAGCCCCTG TACTGGATTACAGCATATTCTCATCTCTGGCCCCGAGGCTGCCTGTGGGGCGAGTGG AGACCTCCCATCACTGAGACAGATCACAGACCACGAGTGCCTTTCCCGGACCTGGAC GTTGCCTCCAAAACAGGCACCAGCTCTTTCCCTCTCTAGACAGAAATATTTTTGTAA GGTTCTGGGGCAGGGAGCATGAAGTACGAGGAAAACTTGAATTCCAGATTTT TAATGCAAAGTATTTATCATTTCTACCAGAAATAAACGTTTTAAGTTTTTACTTGACT AATGAGACCCAGAGTTTGGAGAAAACTTTTGGCCAATGCTGCCACCTGATGTCAGA AAGTGTCCCCACACCCTAGCAGTGGCCTATCTTGGAACAAGAACTTCGAAAGCACCT

FIGURE 1 (continued)

MRLPGVPLARPALLLLLPLLAPLLGTGAPAELRVRVRLPDGQVTEESLQADSDADSISLEL RKPDGTLVSFTADFKKDVKVFRALILGELEKGQSQFQALCFVTQLQHNEIIPSEAMAKLR QKNPRAVRQAEEVRGLEHLHMDVAVNFSQGALLSPHLHNVCAEAVDAIYTRQEDVRF WLEQGVDSSVFEALPKASEQAELPRCRQVGDRGKPCVCHYGLSLAWYPCMLKYCHSR DRPTPYKCGIRSCQKSYSFDFYVPQRQLCLWDEDPYPG*

SEQ ID NO:3

FIGURE 3

 ${\tt MRLPGVPLARPALLLLLPLLAPLLG\ TGAPA}$

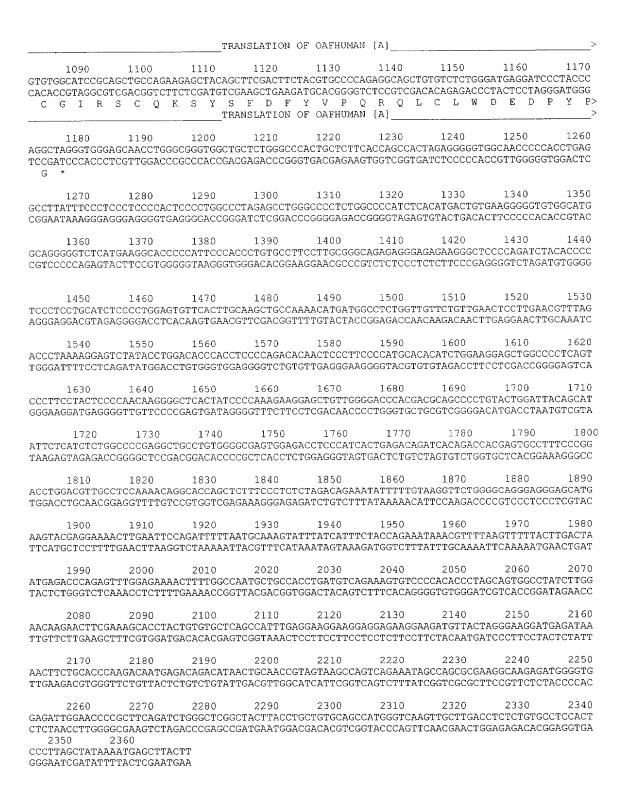
Sequence Range: 1 to 2366

FIGURE 4

2.0 130 140 150 AAACACAGGCTCGCAGCGCTGGAGCCCGGGGCCGCGAGCCGGGCCGGGCCAGCCCTCTCCGCCTCGGGGCCGCCGGGGCCCCTCGC ACTCGCGATGGGTGCACGCAGGCGCGGTGGAGCGCCCGCTGGGGCCCGGTTCCGGGGGGCCCGCCGAGGGCCCGCGGGGCTTGATC ${\tt GGGGGTTGAAACCGCTTCAAACGGACGCGGAGAGGGGCGGGGGTGCGCCGCGCGCCCTGCCGTCGCCGGGGGCCCCTACGC}$ SEO ID NO:2 TRANSLATION OF OAFHUMAN [A] L P G V P L A R P A L L L L P L L A P L L G T G A P A E L> TRANSLATION OF OAFHUMAN [A] CGCCCAGGCGCACGCCGACGGCCTGCCGGTCCACTGGCTCCTCTCGGACGTCCGCCTGTCGCTGCCGCTGTCGTAGTCGGAGCTCGACGC TRANSLATION OF OAFHUMAN [A] GTTCGGGCTGCCGTGGGAGCAGAGGAAGTGGCGGCTGAAGTTCTTCCTACACTTCCAGAAGGCCCGGGACTAGGACCCCCTCGACCTCTT K P D G T L V S F T A D F K K D V K V F R A L I L G E L E K>
TRANSLATION OF OAFHUMAN [A] ______> GGGGCAGAGTCAGTTCCAGGCCCTCTGCTTTGTCACCCAGCTGCAGCACAATGAGATCATCCCCAGTGAGGCCATGGCCAAGCTCCGGCA $\tt CCCCGTCTCAGTCAAGGTCCGGGAGACGAAACAGTGGGTCGACGTCGTGTTACTCTAGTAGGGGTCACTCCGGTACCGGTTCGAGGCCGT$ GQSQFQALCFVTQLQHNEIIPSEAMAKLRQ> TRANSLATION OF OAFHUMAN [A] GAAAAATCCCCGGGCAGTGCGGCAGGCGGAGGAGGTTCGGGGTCTGGAGCATCTGCACATGGATGTCGCTGTCAACTTCAGCCAGGGGGC $\tt CTTTTTAGGGGCCCGTCACGCCGTCCGCCTCCTACAGCCCCAGACCTCGTAGACGTGTACCTACAGCGACAGTTGAAGTCGGTCCCCCG$ $\texttt{K} \ \ \texttt{N} \ \ \texttt{P} \ \ \texttt{R} \ \ \texttt{A} \ \ \texttt{V} \ \ \texttt{R} \ \ \texttt{Q} \ \ \texttt{A} \ \ \texttt{E} \ \ \texttt{E} \ \ \texttt{V} \ \ \texttt{R} \ \ \texttt{G} \ \ \texttt{L} \ \ \texttt{E} \ \ \texttt{H} \ \ \texttt{L} \ \ \texttt{H} \ \ \texttt{M} \ \ \texttt{D} \ \ \texttt{V} \ \ \texttt{N} \ \ \texttt{F} \ \ \texttt{S} \ \ \texttt{Q} \ \ \texttt{G} \ \ \ \texttt{A} > \\$ TRANSLATION OF OAFHUMAN [A]

	TRANSLATION O	F OAFHUMAN [A]_		>
1000 1010 10	20 1030	1040 1050	1060	1070 1080
GCCCTGCGTCTGCCACTATGGCCTGAGC	CTGGCCTGGTACCCCT	GCATGCTCAAGTACTG	CCACAGCCGCGACCGG	CCCACGCCCTACAA
CGGGACGCAGACGGTGATACCGGACTCG	GACCGGACCATGGGGA	CGTACGAGTTCATGAC	GGTGTCGGCGCTGGCC	GGGTGCGGGATGTT
P C V C H Y G L S	L A W Y P	C M L K Y C	HSRDR	PTPYK>

FIGURE 4 (continued)



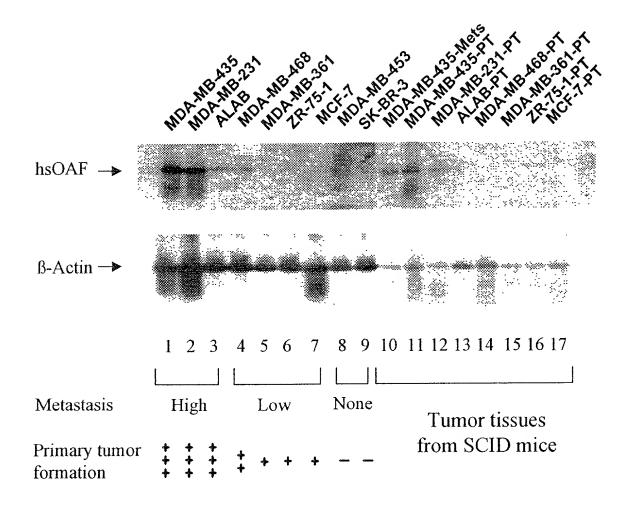


FIGURE 6

MDA-MB-435 soft agar colonies normalized to WST1

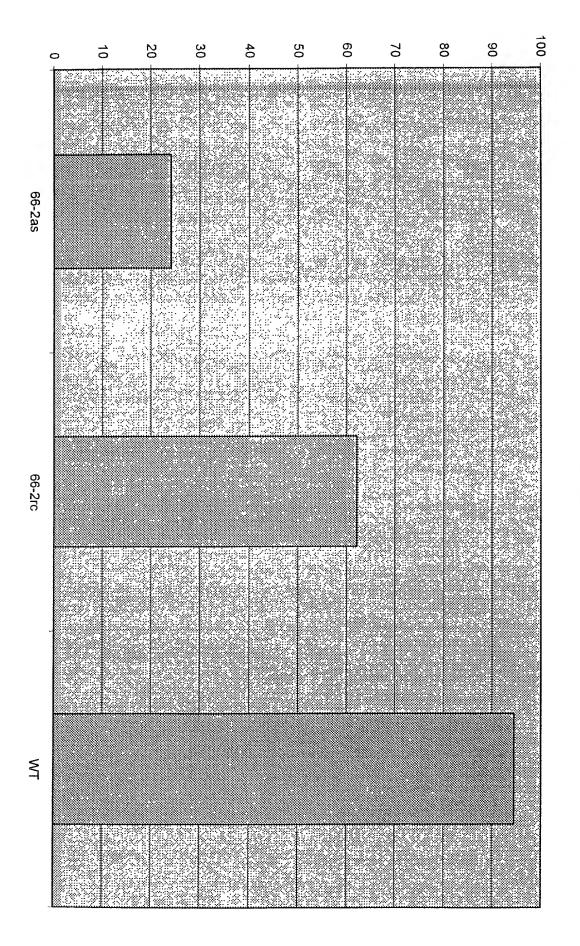
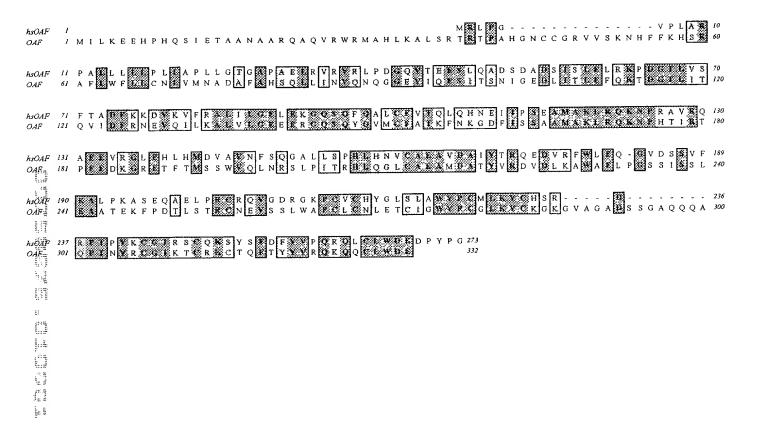


FIGURE 7



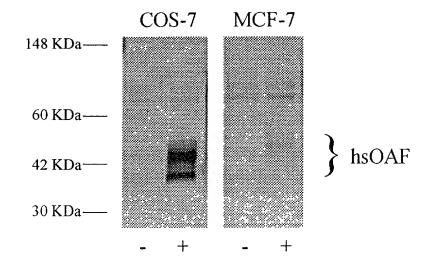
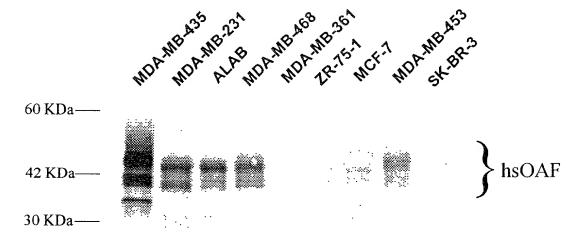
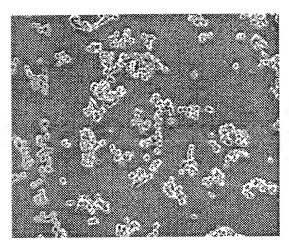


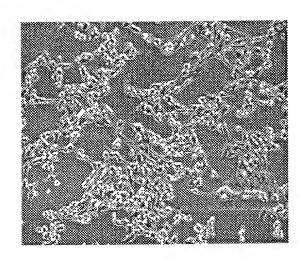
FIGURE 8B



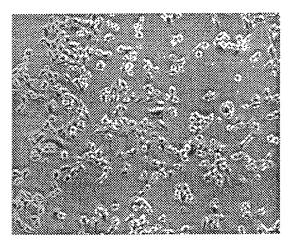
Witached endedandow



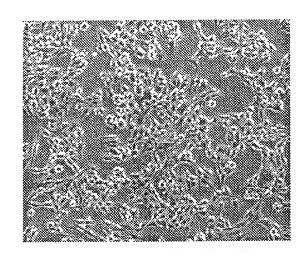




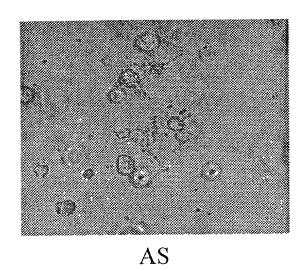
RC

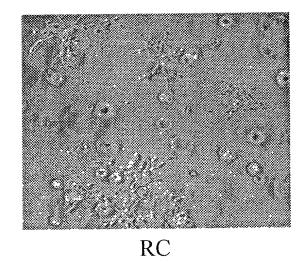


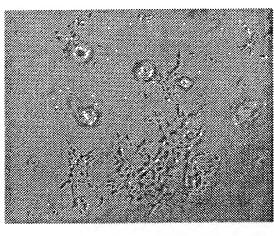
AS+M

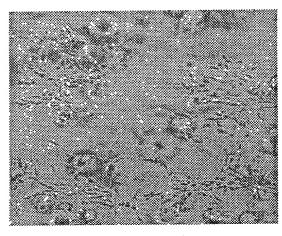


Normal









AS+M

Normal

2339 CTCCCTTAGCTATAAAATGAGCTTACTT-polyA

1 CAAAACACAGGCTCGCAGCGCTGGAGCCCGGGGCCGGAGCCGGGGCCGGGGCAGCGCCGTCTCCGCCTCGGGGCCGCCGGGGGCCCCT GCTGAGCGCTACCCACGTGCGTCCGCGCCACCTCGCGGGCGACCCCGCGGCCAAGGCCCCCGGGGGGCGCCCCGAACT 179 M 359 <u>R L P G V P L A R P A L L L L P L L A P L L G</u> T G A P A E CTGCGGGTCCGCGTGCGGCTGCCGGACGCCAGGTGACCGAGGAGAGCCTGCAGGCGGACAGCGACGCGACAGCATCAGCCTCGAGCTG 449 $\texttt{L} \ \texttt{R} \ \texttt{V} \ \texttt{R} \ \texttt{V} \ \texttt{R} \ \texttt{L} \ \texttt{P} \ \texttt{D} \ \texttt{G} \ \texttt{Q} \ \texttt{V} \ \texttt{T} \ \texttt{E} \ \texttt{E} \ \texttt{S} \ \texttt{L} \ \texttt{Q} \ \texttt{A} \ \texttt{D} \ \texttt{S} \ \texttt{D} \ \texttt{A} \ \texttt{D} \ \texttt{S} \ \texttt{I} \ \texttt{S} \ \texttt{L} \ \texttt{E} \ \texttt{L}$ 32 539 R K P D G T L V S F T A D F K K D V K V F R A L I L G E L E 629 K G Q S Q F Q A L C F V T Q L Q H N E I I P S E A M A K L R CAGAAAAATCCCCGGGCAGTGCGGCAGGCGGAGGAGGTTCGGGGTCTGGAGCATCTGCACATGGATGTCGCTGTCAACTTCAGCCAGGGG 719 Q K N P R A V R Q A E E V R G L E H L H M D V A V N F S Q G 809 A L L S P H L H N V C A E A V D A I Y T R Q E D V R F W L E 152 Q G V D S S V F E A L P K A S E Q A E L P R C R Q V G D R G 182 K P C V C H Y G L S L A W Y P C M L K Y C H S R D R P T P Y 212 AAGTGTGGCATCCGCAGCTGCCAGAAGAGCTTACAGCTTCGACTTCTACGTGCCCCAGAGGCAGCTGTGTCTCTGGGATGAGGATCCCTAC 1079 K C G I R S C Q K S Y S F D F Y V P Q R Q L C L W D E D P Y 242 1169 1259 $\tt CCTCCCTCCTGCATCTCCCCTGGAGTGTTCACTTGCAAGCTGCCAAAACATGATGGCCTCTGGTTGTTCTGTTGAACTCCTTGAACGTTT$ GTCCCTTCCTACTCCCCAACAAGGGGCTCACTATCCCCAAAGAAGGAGCTGTTGGGGACCCACGACGCAGCCCCTGTACTGGATTACAGC 1709 GGACCTGGACGTTGCCTCCAAAACAGGCACCAGCTCTTTCCCTCTCTAGACAGAAATATTTTTTGTAAGGTTCTGGGGCAGGAGGAGGAGCA TGAAGTACGAGGAAAACTTGAATTCCAGATTTTTAATGCAAAGTATTTATCATTTCTACCAGAAATAAACGTTTTAAGTTTTTACTTGAC TAATGAGACCCAGAGTTTGGAGAAAACTTTTGGCCAATGCTGCCACCTGATGTCAGAAAGTGTCCCCACACCCTAGCAGTGGCCTATCTT AAAACTTCTGCACCCAAGACAATGAGACAGACATAACTGCAACCGTAGTAAGCCAGTCAGAAATAGCCAGCGCGAAGGCAAGAGATGGGG 2159 2249 ${\tt TGGAGATTGGAACCCCGCTTCAGATCTGGGCTCGGCTACTTACCTGCTGTGCAGCCATGGGTCAAGTTGCTTGACCTCTCTGTGCCTCCAGCTTGAGCTTGAGCTTGAGCTTGAGCTTGAGCTTGAGCTTGAGCTTGAGCTTGAGCTTGAGCTTGAGCTTGAGCTTGAGCTTGAGCTTGAGCTTGAGCTTGAGGGTTGAGGGGTTGAGGGGTTGAGGGGTTGAGGGGTTGAGGGGTTGAGGGGTTGAGGGGTTGAGGGGTTGAGGGGTTAGGGGGTTGAGGGGTTAGGGGTTGAGGGGTTGAGGGGTTGAGGGGTTGAGGG$

FIGURE 12A

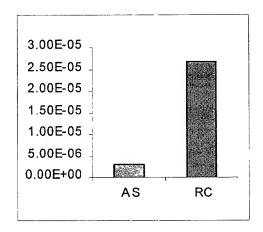


FIGURE 12B

